

SEQUENCE LISTING

<110> Jackson, W. James
Pace, John

<120> Chlamydia Protein, Gene Sequence and Uses Thereof

<130> 7969-086-999

<140> 09/612,402

<141> 2000-07-06

<150> 08/942,596

<151> 1997-10-02

<160> 43

<170> PatentIn version 3.0

<210> 1

<211> 4435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

<220>

<221> CDS

<222> (382)..(3417)

<223>

<400> 1

gggcaaaact cttccccccg ggatttatat gggaaagggg aaactttggc ccgtattcaa	60
gcgccacggg ttttggggcg gaatgaattt tttcgttccg gaaaaagtaa ttccccggga	120
acgtagggtg tcggtttcat aggctcgcca aatgggatag aggtggaaag gtaaaaaaaaa	180
ctgagccaag caaaggatag agaagtcctg taatcatcgc aggttaaagg ggggatgtta	240
ttttagcctg caaatagtg t aattattgga tcctgtaaag agaaaaggac gaatgcgctg	300
aagataagaa cattttattga tattaaatta ttaatttttt atgaagcggg gtaattaatt	360
ttatctctca gcttttgtgt g atg caa acg tct ttc cat aag ttc ttt ctt	411
Met Gln Thr Ser Phe His Lys Phe Phe Leu	
1 5 10	
tca atg att cta gct tat tct tgc tgc tct tta aat ggg ggg gga tat	459
Ser Met Ile Leu Ala Tyr Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr	
15 20 25	
gca gca gaa atc atg gtt cct caa gga att tac gat ggg gag acg tta	507
Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu	
30 35 40	
act gta tca ttt ccc tat act gtt ata gga gat ccg agt ggg act act	555
Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr	
45 50 55	
gtt ttt tct gca gga gag tta aca tta aaa aat ctt gac aat tct att	603
Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile	
60 65 70	
gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act	651
Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr	
75 80 85 90	
gtt tta ggg aga gga cac tcg ttg act ttc gag aac ata cgg act tct	699
Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser	
95 100 105	

aca aat ggg gca gct cta agt aat agc gct gct gat gga ctg ttt act	747
Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr	
110 115 120	
att gag ggt ttt aaa gaa tta tcc ttt tcc aat tgc aat tca tta ctt	795
Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu	
125 130 135	
gcc gta ctg cct gct gca acg act aat aag ggt agc cag act ccg acg	843
Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr	
140 145 150	
aca aca tct aca ccg tct aat ggt act att tat tct aaa aca gat ctt	891
Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu	
155 160 165 170	
ttg tta ctc aat aat gag aag ttc tca ttc tat agt aat tta gtc tct	939
Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser	
175 180 185	
gga gat ggg gga gct ata gat gct aag agc tta acg gtt caa gga att	987
Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile	
190 195 200	
agc aag ctt tgt gtc ttc caa gaa aat act gct caa gct gat ggg gga	1035
Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly	
205 210 215	
gct tgt caa gta gtc acc agt ttc tct gct atg gct aac gag gct cct	1083
Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro	
220 225 230	
att gcc ttt gta gcg aat gtt gca gga gta aga ggg gga ggg att gct	1131
Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala	
235 240 245 250	
gct gtt cag gat ggg cag cag gga gtg tca tca tct act tca aca gaa	1179
Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu	
255 260 265	
gat cca gta gta agt ttt tcc aga aat act gcg gta gag ttt gat ggg	1227
Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly	
270 275 280	
aac gta gcc cga gta gga gga ggg att tac tcc tac ggg aac gtt gct	1275
Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala	
285 290 295	
ttc ctg aat aat gga aaa acc ttg ttt ctc aac aat gtt gct tct cct	1323
Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro	
300 305 310	
gtt tac att gct gct aag caa cca aca agt gga cag gct tct aat acg	1371
Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr	
315 320 325 330	
agt aat aat tac gga gat gga gga gct atc ttc tgt aag aat ggt gcg	1419
Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala	
335 340 345	
caa gca gga tcc aat aac tct gga tca gtt tcc ttt gat gga gag gga	1467
Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly	
350 355 360	
gta gtt ttc ttt agt agc aat gta gct gct ggg aaa ggg gga gct att	1515
Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile	
365 370 375	
tat gcc aaa aag ctc tcg gtt gct aac tgt ggc cct gta caa ttt tta	1563
Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu	
380 385 390	
agg aat atc gct aat gat ggt gga gcg att tat tta gga gaa tct gga	1611
Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly	
395 400 405 410	
gag ctc agt tta tct gct gat tat gga gat att att ttc gat ggg aat	1659
Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn	
415 420 425	

ctt	aaa	aga	aca	gcc	aaa	gag	aat	gct	gcc	gat	gtt	aat	ggc	gta	act	1707
Leu	Lys	Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	
			430					435					440			
gtg	tcc	tca	caa	gcc	att	tcg	atg	gga	tcg	gga	ggg	aaa	ata	acg	aca	1755
Val	Ser	Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	
		445					450					455				
tta	aga	gct	aaa	gca	ggg	cat	cag	att	ctc	ttt	aat	gat	ccc	atc	gag	1803
Leu	Arg	Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	
	460				465				470							
atg	gca	aac	gga	aat	aac	cag	cca	gcg	cag	tct	tcc	aaa	ctt	cta	aaa	1851
Met	Ala	Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu	Leu	Lys	
	475				480					485					490	
att	aac	gat	ggt	gaa	gga	tac	aca	ggg	gat	att	gtt	ttt	gct	aat	gga	1899
Ile	Asn	Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	
			495					500					505			
agc	agt	act	ttg	tac	caa	aat	gtt	acg	ata	gag	caa	gga	agg	att	gtt	1947
Ser	Ser	Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	
			510					515					520			
ctt	cgt	gaa	aag	gca	aaa	tta	tca	gtg	aat	tct	cta	agt	cag	aca	ggt	1995
Leu	Arg	Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	
		525					530					535				
ggg	agt	ctg	tat	atg	gaa	gct	ggg	agt	aca	tgg	gat	ttt	gta	act	cca	2043
Gly	Ser	Leu	Tyr	Met	Glu	Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val	Thr	Pro	
	540				545					550						
caa	cca	cca	caa	cag	cct	cct	gcc	gct	aat	cag	ttg	atc	acg	ctt	tcc	2091
Gln	Pro	Pro	Gln	Gln	Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	
	555				560					565					570	
aat	ctg	cat	ttg	tct	ctt	tct	tct	ttg	tta	gca	aac	aat	gca	gtt	acg	2139
Asn	Leu	His	Leu	Ser	Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	
			575					580						585		
aat	cct	cct	acc	aat	cct	cca	gcg	caa	gat	tct	cat	cct	gca	gtc	att	2187
Asn	Pro	Pro	Thr	Asn	Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	
			590					595					600			
ggt	agc	aca	act	gct	ggt	tct	gtt	aca	att	agt	ggg	cct	atc	ttt	ttt	2235
Gly	Ser	Thr	Thr	Ala	Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	
		605					610					615				
gag	gat	ttg	gat	gat	aca	gct	tat	gat	agg	tat	gat	tgg	cta	ggt	tct	2283
Glu	Asp	Leu	Asp	Asp	Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	
		620				625					630					
aat	caa	aaa	atc	aat	gtc	ctg	aaa	tta	cag	tta	ggg	act	aag	ccc	cca	2331
Asn	Gln	Lys	Ile	Asn	Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys	Pro	Pro	
					640				645					650		
gct	aat	gcc	cca	tca	gat	ttg	act	cta	ggg	aat	gag	atg	cct	aag	tat	2379
Ala	Asn	Ala	Pro	Ser	Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	
			655					660					665			
ggc	tat	caa	gga	agc	tgg	aag	ctt	gcg	tgg	gat	cct	aat	aca	gca	aat	2427
Gly	Tyr	Gln	Gly	Ser	Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	
			670					675					680			
aat	ggt	cct	tat	act	ctg	aaa	gct	aca	tgg	act	aaa	act	ggg	tat	aat	2475
Asn	Gly	Pro	Tyr	Thr	Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	
		685					690					695				
cct	ggg	cct	gag	cga	gta	gct	tct	ttg	gtt	cca	aat	agt	tta	tgg	gga	2523
Pro	Gly	Pro	Glu	Arg	Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	
		700				705					710					
tcc	att	tta	gat	ata	cga	tct	gcg	cat	tca	gca	att	caa	gca	agt	gtg	2571
Ser	Ile	Leu	Asp	Ile	Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	
					720				725						730	
gat	ggg	cgc	tct	tat	tgt	cga	gga	tta	tgg	gtt	tct	gga	gtt	tcg	aat	2619
Asp	Gly	Arg	Ser	Tyr	Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	
				735					740					745		

ttc ttc tat cat gac cgc gat gct tta ggt cag gga tat cgg tat att	2667
Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile	
750 755 760	
agt ggg ggt tat tcc tta gga gca aac tcc tac ttt gga tca tcg atg	2715
Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met	
765 770 775	
ttt ggt cta gca ttt acc gaa gta ttt ggt aga tct aaa gat tat gta	2763
Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val	
780 785 790	
gtg tgt cgt tcc aat cat cat gct tgc ata gga tcc gtt tat cta tct	2811
Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser	
795 800 805 810	
acc caa caa gct tta tgt gga tcc tat ttg ttc gga gat gcg ttt atc	2859
Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile	
815 820 825	
cgt gct agc tac ggg ttt ggg aat cag cat atg aaa acc tca tat aca	2907
Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr	
830 835 840	
ttt gca gag gag agc gat gtt cgt tgg gat aat aac tgt ctg gct gga	2955
Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly	
845 850 855	
gag att gga gcg gga tta ccg att gtg att act cca tct aag ctc tat	3003
Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr	
860 865 870	
ttg aat gag ttg cgt cct ttc gtg caa gct gag ttt tct tat gcc gat	3051
Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp	
875 880 885 890	
cat gaa tct ttt aca gag gaa ggc gat caa gct cgg gca ttc aag agc	3099
His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser	
895 900 905	
gga cat ctc cta aat cta tca gtt cct gtt gga gtg aag ttt gat cga	3147
Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg	
910 915 920	
tgt tct agt aca cat cct aat aaa tat agc ttt atg gcg gct tat atc	3195
Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile	
925 930 935	
tgt gat gct tat cgc acc atc tct ggt act gag aca acg ctc cta tcc	3243
Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser	
940 945 950	
cat caa gag aca tgg aca aca gat gcc ttt cat tta gca aga cat gga	3291
His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly	
955 960 965 970	
gtt gtg gtt aga gga tct atg tat gct tct cta aca agt aat ata gaa	3339
Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu	
975 980 985	
gta tat ggc cat gga aga tat gag tat cga gat gct tct cga ggc tat	3387
Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr	
990 995 1000	
ggt ttg agt gca gga agt aga gtc cgg ttc taaaaatatt ggtagatag	3437
Gly Leu Ser Ala Gly Ser Arg Val Arg Phe	
1005 1010	
ttaagtgtta gcgatgcctt tttctttgag atctacatca ttttggtttt tagcttggtt	3497
gtgttctcat tcgtatggat tcgcgagctc tctcgaagtg ttaacgccta atgtaaccac	3557
tctttttaag ggagacgat tttacttgaa tggagactgc gcttttgatca atgtctatgc	3617
aggagctgaa gaaggttcga ttatctcagc taatggcgac aatttaacga ttaccggaca	3677
aaaccataca ttatcattta cagattctca agggccagtt cttcaaaatt atgccttcat	3737
ttcagcagga gagacactta ctctgagaga tttttcgagt ctgatgttct cgaaaaatgt	3797
ttcttgcgga gaaaagggaa tgatctccgg gaaaaccgtg agtatttccg gagcaggcga	3857
agtgattttc tgggataact ccgtggggta ttctccttta tctactgtgc caacctcatc	3917
atcaactccg cctgctccaa cagttagtga tgctcggaata ggggtctattt tttctgtaga	3977
gactagtttg gagatctcag gcgtcaaaaa aggggtcatg ttcgataata atgccgggaa	4037
tttcggaaca gtttttcgag gtaagaataa taataatgct ggtggtggag gcagtgggtt	4097

ccgctacacc	atcaagtacg	actttttacag	ttaaaaaactg	taaagggaaa	gtttctttca	4157
cagataacgt	agcctcttgc	ggaggcggag	tggttttataa	aggcattgtg	cttttcaaag	4217
acaatgaagg	aggcatattc	ttccgagggg	acacagcata	cgatgattta	aggattcttg	4277
ctgctactaa	tcaggatcag	aatacggaga	caggaggcgg	tggaggagtt	atttgctctc	4337
cagatgattc	tgtaaagttt	gaaggcaata	aaggttctat	tgtttttgat	tacaactttg	4397
caaaaggcag	aggcggaagc	atcctaacga	aagaattc			4435

<210> 2
 <211> 1012
 <212> PRT
 <213> Chlamydia sp.

<400> 2

Met	Gln	Thr	Ser	Phe	His	Lys	Phe	Phe	Leu	Ser	Met	Ile	Leu	Ala	Tyr
1				5					10					15	
Ser	Cys	Cys	Ser	Leu	Asn	Gly	Gly	Gly	Tyr	Ala	Ala	Glu	Ile	Met	Val
			20					25					30		
Pro	Gln	Gly	Ile	Tyr	Asp	Gly	Glu	Thr	Leu	Thr	Val	Ser	Phe	Pro	Tyr
		35					40					45			
Thr	Val	Ile	Gly	Asp	Pro	Ser	Gly	Thr	Thr	Val	Phe	Ser	Ala	Gly	Glu
	50					55					60				
Leu	Thr	Leu	Lys	Asn	Leu	Asp	Asn	Ser	Ile	Ala	Ala	Leu	Pro	Leu	Ser
65				70					75					80	
Cys	Phe	Gly	Asn	Leu	Leu	Gly	Ser	Phe	Thr	Val	Leu	Gly	Arg	Gly	His
			85					90					95		
Ser	Leu	Thr	Phe	Glu	Asn	Ile	Arg	Thr	Ser	Thr	Asn	Gly	Ala	Ala	Leu
			100					105					110		
Ser	Asn	Ser	Ala	Ala	Asp	Gly	Leu	Phe	Thr	Ile	Glu	Gly	Phe	Lys	Glu
		115					120					125			
Leu	Ser	Phe	Ser	Asn	Cys	Asn	Ser	Leu	Leu	Ala	Val	Leu	Pro	Ala	Ala
	130					135					140				
Thr	Thr	Asn	Lys	Gly	Ser	Gln	Thr	Pro	Thr	Thr	Ser	Thr	Pro	Ser	
145					150					155				160	
Asn	Gly	Thr	Ile	Tyr	Ser	Lys	Thr	Asp	Leu	Leu	Leu	Leu	Asn	Asn	Glu
			165					170						175	
Lys	Phe	Ser	Phe	Tyr	Ser	Asn	Leu	Val	Ser	Gly	Asp	Gly	Gly	Ala	Ile
			180					185					190		
Asp	Ala	Lys	Ser	Leu	Thr	Val	Gln	Gly	Ile	Ser	Lys	Leu	Cys	Val	Phe
		195					200					205			
Gln	Glu	Asn	Thr	Ala	Gln	Ala	Asp	Gly	Gly	Ala	Cys	Gln	Val	Val	Thr
	210					215					220				
Ser	Phe	Ser	Ala	Met	Ala	Asn	Glu	Ala	Pro	Ile	Ala	Phe	Val	Ala	Asn
225					230					235					240
Val	Ala	Gly	Val	Arg	Gly	Gly	Gly	Ile	Ala	Ala	Val	Gln	Asp	Gly	Gln
			245					250						255	
Gln	Gly	Val	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	Phe	
		260					265						270		
Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	Gly
		275					280					285			
Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys
	290					295					300				
Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr	Ile	Ala	Ala	Lys
305					310					315					320
Gln	Pro	Thr	Ser	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asn	Asn	Tyr	Gly	Asp
			325						330					335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Gly	Ser	Asn	Asn
		340						345					350		
Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser	Ser
		355					360					365			
Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Ser
	370					375					380				

Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn	Ile	Ala	Asn	Asp
385					390					395					400
Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser	Ala
			405						410					415	
Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala	Lys
			420					425					430		
Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala	Ile
		435					440					445			
Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala	Gly
	450					455					460				
His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn	Asn
465					470					475					480
Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu	Leu	Lys	Ile	Asn	Asp	Gly	Glu	Gly
				485					490					495	
Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Ser	Ser	Thr	Leu	Tyr	Gln
			500					505					510		
Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala	Lys
		515					520					525			
Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met	Glu
	530					535					540				
Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln	Pro
545					550					555					560
Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser	Leu
				565					570					575	
Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn	Pro
			580					585					590		
Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala	Gly
		595					600					605			
Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp	Leu	Asp	Asp	Thr
	610					615					620				
Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asn	Val
625					630					635					640
Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys	Pro	Pro	Ala	Asn	Ala	Pro	Ser	Asp
				645					650					655	
Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser	Trp
		660						665					670		
Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr	Leu
		675					680					685			
Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg	Val
	690					695					700				
Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile	Arg
705					710					715					720
Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr	Cys
				725					730					735	
Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp	Arg
			740					745					750		
Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser	Leu
		755					760					765			
Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe	Thr
	770					775					780				
Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn	His
785					790					795					800
His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Gln	Gln	Ala	Leu	Cys
				805					810					815	
Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly	Phe
			820					825					830		
Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser	Asp
		835					840					845			
Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Ala	Gly	Glu	Ile	Gly	Ala	Gly	Leu
	850					855					860				
Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn	Glu	Leu	Arg	Pro
865					870					875					880

[illegible]

<212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 12, 15
 <223> n = a, t, g, or c

 <400> 6
 gagathatgg tnccncaa 18

 <210> 7
 <211> 18
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 12, 15
 <223> n = a, t, g, or c

 <400> 7
 gagathatgg tnccncag 18

 <210> 8
 <211> 15
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 1, 7
 <223> n = a, t, g, or c

 <400> 8
 ngtytcnccr tcata 15

 <210> 9
 <211> 15
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 1, 7
 <223> n = a, t, g, or c

 <400> 9
 ngtytcnccr tcgta 15

 <210> 10
 <211> 1511
 <212> DNA
 <213> Chlamydia sp.

 <400> 10
 gaaatcatgg ttcctcaagg aattttacgat ggggagacgt taactgtatc atttccctat 60
 actgttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaataa 120
 aatcttgaca attctattgc agctttgcct ttaagttggt ttgggaactt attagggagt 180
 tttactgttt tagggagagg acactcgttg actttcgaga acatacggac ttctacaaat 240
 ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300
 ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360

ggtagccaga	ctccgacgac	aacatctaca	ccgtctaattg	gtactatttta	ttctaaaaca	420
gatcttttgt	tactcaataa	tgagaagttc	tcattctata	gtaatttagt	ctctggagat	480
gggggagcta	tagatgctaa	gagcttaacg	gttcaaggaa	ttagcaagct	ttgtgtcttc	540
caagaaaata	ctgctcaagc	tgatggggga	gcttgtcaag	tagtcaccag	tttctctgct	600
atggctaacg	aggctcctat	tgcccttgta	gcgaatgttg	caggagtaag	agggggaggg	660
attgctgctg	ttcaggatgg	gcagcaggga	gtgtcatcat	ctacttcaac	agaagatcca	720
gtagtaagtt	tttccagaaa	tactgcggtg	gagtttgatg	ggaacgtagc	ccgagtagga	780
ggagggattt	actcctacgg	gaacgttgct	ttcctgaata	atggaaaaac	cttgtttctc	840
aacaatgttg	cttctcctgt	ttacattgct	gctaagcaac	caacaagtgg	acaggcttct	900
aatacgagta	ataattacgg	agatggagga	gctatcttct	gtaagaatgg	tgcgcaagca	960
ggatccaata	actctggatc	agtttccttt	gatggagagg	gagtagtttt	ctttagtagc	1020
aatgtagctg	ctgggaaagg	gggagctatt	tatgccaaaa	agctctcggt	tgctaactgt	1080
ggccctgtac	aattttttaag	gaatatcgct	aatgatgggtg	gagcgattta	tttaggagaa	1140
tctggagagc	tcagtttatc	tgctgattat	ggagatatta	ttttcgatgg	gaatccttaa	1200
agaacagcca	aagagaatgc	tgccgatgtt	aatggcgtaa	ctgtgtctct	acaagccatt	1260
tcgatgggat	cgggagggaa	aataacgaca	ttaagagcta	aagcagggca	tcagattctc	1320
tttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgcagtc	ttccaaactt	1380
ctaaaaatta	acgatgggtg	aggatacaca	ggggatattg	tttttgctaa	tggaagcagt	1440
actttgtacc	aaaatgttac	gatagagcaa	ggaaggattg	ttcttcgtga	aaaggcaaaa	1500
ttatcagtga	a					1511

<210> 11
 <211> 1444
 <212> DNA
 <213> Chlamydia sp.

<400> 11						
ttctctaagt	cagacaggtg	ggagtctgta	tatggaagct	gggagtacat	gggattttgt	60
aactccacaa	ccaccacaac	agcctcctgc	cgctaatacag	ttgatcacgc	tttccaatct	120
gcatttgtct	ctttcttctt	tgtagcaaaa	caatgcagtt	acgaatcctc	ctaccaatcc	180
tccagcgcaa	gattctcatc	ctgcagtcac	tggtagcaca	actgctgggt	ctgttacaat	240
tagtgggcct	atcttttttg	aggattttgga	tgatacacgt	tatgataggt	atgattggct	300
aggttctaata	caaaaaatca	atgtcctgaa	attacagtta	gggactaagc	ccccagctaa	360
tgccccatca	gatttgactc	tagggaatga	gatgcctaag	tatggctatc	aaggaagctg	420
gaagcttgcg	tgggattccta	atacagcaaa	taatggctct	tatactctga	aagctacatg	480
gactaaaact	gggtataatc	ctgggcctga	gcgagtagct	tctttgggtc	caaatagttt	540
atggggatcc	attttagata	tacgatctgc	gcattcagca	attcaagcaa	gtgtggatgg	600
gcgctcttat	tgctcaggat	tatgggtttc	tggagtttcg	aatttcttct	atcatgaccg	660
cgatgcttta	ggtcagggat	atcggtatat	tagtgggggt	tattccttag	gagcaaactc	720
ctactttgga	tcacgatgtg	ttggtctagc	atttaccgaa	gtatttggtg	gatctaaaga	780
ttatgtagtg	tgctggttcca	atcatcatgc	ttgcatagga	tccgtttatc	tatctacca	840
acaagcttta	tgtggatcct	atltgttcgg	agatgcgttt	atccgtgcta	gctacgggtt	900
tggaatcag	catatgaaaa	cctcatatac	atltgcagag	gagagcgatg	ttcgttggga	960
taataactgt	ctggctggag	agattggagc	gggattaccg	attgtgatta	ctccatctaa	1020
gctctatttg	aatgagttgc	gtcctttcgt	gcaagctgag	ttttcttatg	ccgatcatga	1080
atcttttaca	gaggaaggcg	atcaagctcg	ggcattcaag	agcggacatc	tcctaaatct	1140
atcagttcct	gttgagtgga	agtttgatcg	atgttctagt	acacatccta	ataaatatag	1200
ctttatggcg	gcttatatct	gtgatgctta	tcgcaccatc	tctggtactg	agacaacgct	1260
cctatcccat	caagagacat	ggacaacaga	tgcccttcat	ttagcaagac	atggagttgt	1320
ggtagagga	tctatgtatg	cttctctaac	aagtaataata	gaagtatatg	gccatggaag	1380
atatgagtat	cgagatgctt	ctcgaggcta	tggtttgagt	gcaggaagta	gagtcgggtt	1440
ctaa						1444

<210> 12
 <211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 12						
aagggcccaa	ttacgcagag	ggtaccgaaa	ttatggttcc	tcaaggaatt	tacgat	56

<210> 13

<211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 13
 aagggcccaa ttacgcagag ggtaccctaa gaagaaggca tgccgtgcta gcggag 56

<210> 14
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 14
 aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 15
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn
 225 230 235 240
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
 245 250 255
 Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe
 260 265 270
 Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly
 275 280 285
 Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys
 290 295 300
 Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu
 305 310 315 320

Cys Gly Ser Tyr Val Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 835 840 845
 Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 16
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 16
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Thr Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220

Ser	Phe	Ser	Ala	Met	Ala	Asn	Glu	Ala	Pro	Ile	Ala	Phe	Ile	Ala	Asn
225					230					235					240
Val	Ala	Gly	Val	Arg	Gly	Gly	Gly	Ile	Ala	Ala	Val	Gln	Asp	Gly	Gln
				245					250					255	
Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	Phe
			260					265					270		
Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	Gly
		275					280					285			
Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys
	290					295					300				
Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr	Ile	Ala	Ala	Glu
305					310					315					320
Gln	Pro	Thr	Asn	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asp	Asn	Tyr	Gly	Asp
				325					330					335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Ala	Gly	Ser	Asn
			340					345					350		
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		355					360					365			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
	370					375					380				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Gly	Asn	Ile	Ala	Asn
385					390					395					400
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
				405				410						415	
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala
			420					425					430		
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala
		435					440					445			
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala
	450					455					460				
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn
465					470					475					480
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu
				485					490					495	
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr
			500					505					510		
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala
		515					520					525			
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met
	530					535					540				
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln
545					550					555					560
Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser
				565					570					575	
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn
			580					585					590		
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala
		595					600					605			
Gly	Pro	Val	Thr	Ile	Ser	Gly	Pro	Phe	Phe	Phe	Glu	Asp	Leu	Asp	Asp
	610					615					620				
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp
625					630					635					640
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Ser	Ala	Asn	Ala	Pro	Ser
				645					650					655	
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser
			660					665					670		
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr
		675					680					685			
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg
	690					695					700				
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile
705					710					715					720

Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 725 730 735
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Ser Tyr His Asp
 740 745 750
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 755 760 765
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 770 775 780
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 785 790 795 800
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Lys Gln Ala Leu
 805 810 815
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 835 840 845
 Asp Val Arg Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Thr Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 17
 <211> 505
 <212> PRT
 <213> Chlamydia sp.

<400> 17
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
 1 5 10 15
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125

Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala
 340 345 350
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn
 355 360 365
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys
 385 390 395 400
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser
 405 410 415
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg
 420 425 430
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala
 435 440 445
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn
 450 455 460
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser
 465 470 475 480
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg
 485 490 495
 Glu Lys Ala Lys Leu Ser Val Asn Ser
 500 505

<210> 18
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 18
 aagggcccaa ttacgcagag ctcgagagaa attatgggttc ctcaaggaat ttacgat

57

<210> 19
 <211> 20
 <212> DNA
 <213> Chlamydia sp.

<400> 19
cgctctagaa ctagtgatc 20

<210> 20
<211> 22
<212> DNA
<213> Chlamydia sp.

<400> 20
atgggttcctc aaggaattta cg 22

<210> 21
<211> 19
<212> DNA
<213> Chlamydia sp.

<400> 21
ggtcccccat cagcgggag 19

<210> 22
<211> 1515
<212> DNA
<213> Chlamydia sp.

<400> 22
gaaatcatgg ttcctcaagg aattttacgat ggggagacgt taactgtatc atttccttat 60
actgttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaaaa 120
aatcttgaca attctattgc agctttgcct ttaagtgtt ttgggaactt attagggagt 180
tttactgttt tagggagagg acaactcggtg actttcgaga acatacggac ttctacaaat 240
ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300
ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360
ggtagccaga ctccgacgac aacatctaca ccgtctaata gtactattta ttctaaaaca 420
gatcttttgt tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat 480
gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc 540
caagaaaata ctgctcaagc tgatggggga gcttggtcaag tagtcaccag tttctctgct 600
atggctaacg aggctcctat tgcctttgta gcgaatgttg caggagtaag agggggaggg 660
attgctgctg ttcaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca 720
gtagtaagtt tttccagaaa tactgcggtg gagtttgatg ggaacgtagc ccgagtagga 780
ggagggattt actcctacgg gaacgttgct ttcctgaata atggaaaaaac cttgtttctc 840
aacaatgttg cttctcctgt ttacattgct gctaagcaac caacaagtgg acaggcttct 900
aatacgagta ataattacgg agatggagga gctatcttct gtaagaatgg tgcgcaagca 960
ggatccaata actctggatc agtttctctt gatggagagg gagtagtttt ctttagtagc 1020
aatgtagctg ctgggaaagg gggagctatt tatgccaaaa agctctcggg tgctaactgt 1080
ggccctgtac aattttttaag gaatatcgct aatgatggtg gagcgattta tttaggagaa 1140
tctggagagc tcagtttatc tgctgattat ggagatatta ttttcgatgg gaatcttaaa 1200
agaacagcca aagagaatgc tgccgatgtt aatggcgtaa ctgtgtcctc acaagccatt 1260
tcgatgggat cgggagggaa aataacgaca ttaagagcta aagcagggca tcagattctc 1320
tttaatgata ccatcgagat ggcaaacgga aataaccagc cagcgagtc ttccaaactt 1380
ctaaaaatta acgatggtga aggatacaca ggggatattg tttttgctaa tggaagcagt 1440
actttgtacc aaaatgttac gatagagcaa ggaaggattg ttcttcgtga aaaggcaaaa 1500
ttatcagtga attct 1515

<210> 23
<211> 3354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 23
atgcaaacgt ctttccataa gttctttctt tcaatgattc tagcttattc ttgctgctct 60

ttaaattgggg	ggggggtatgc	agaaatcatg	gttcctcaag	gaattttacga	tgggggagacg	120
ttaactgtat	cattttcccta	tactgttata	ggagatccga	gtgggactac	tgttttttct	180
gcaggagagt	taacgtttaa	aaatcttgac	aattctattg	cagctttgcc	tttaagtgtg	240
tttgggaact	tattagggag	ttttactggt	ttagggagag	gacactcggt	gacttttcgag	300
aacatacgga	cttctacaaa	tggagctgca	ctaagtgaca	gcgctaatag	cgggttattt	360
actattgagg	gtttttaaaga	attatctttt	tccaattgca	acccattact	tgccgtactg	420
cctgctgcaa	cgactaataa	tggtagccag	actccgtcga	caacatctac	accgttctaat	480
ggtactattt	attctaaaaac	agatcttttg	ttactcaata	atgagaagtt	ctcattctat	540
agtaattcag	tctctggaga	tgggggagct	atagatgcta	agagcttaac	ggttcaagga	600
attagcaagc	tttgtgtctt	ccaagaaaat	actgctcaag	ctgatggggg	agcttgtcaa	660
gtagtcacca	gtttctctgc	tatggctaac	gaggctccta	ttgcctttgt	agcgaatgtt	720
gcaggagtaa	gagggggagg	gattgctgct	gttcaggatg	ggcagcaggg	agtgtcatca	780
tctacttcaa	cagaagatcc	agtagtaagt	ttttccagaa	atactgcggt	agagtttgat	840
gggaacgtag	cccagtagtag	aggagggatt	tactcctacg	ggaacgttgc	tttcctgaat	900
aatggaaaaa	ccttggtttct	caacaatggt	gcttctcctg	tttacattgc	tgctgagcaa	960
ccaacaaatg	gacaggcttc	taatacgagt	gataattacg	gagatggagg	agctatcttc	1020
tgtagaatg	gtgcgcaagc	agcaggatcc	aataactctg	gatcagtttc	ctttgatgga	1080
gagggagtag	ttttcttttag	tagcaatgta	gctgctggga	aagggggagc	tatttatgcc	1140
aaaaagctct	cggttgctaa	ctgtggccct	gtacaactct	tagggaatat	cgctaatagat	1200
ggtggagcga	tttatattag	agaatctgga	gagctcagtt	tatctgctga	ttatggagat	1260
atgatttttc	atgggaatct	taaaagaaca	gcaaagaga	atgctgccga	tgtaattggc	1320
gtaacttgtgt	cctcacaaagc	catttcgatg	ggatcgggag	ggaaaataac	gacattaaga	1380
gctaaagcag	ggcatcagat	tctctttaat	gatcccatcg	agatggcaaa	cggaaataac	1440
cagccagcgc	agtcttccga	acctctaaaa	attaacgatg	gtgaaggata	cacaggggat	1500
attgtttttg	ctaattggaaa	cagtactttg	taccaaagt	ttacgataga	gcaagggaag	1560
attgttcttc	gtgaaaaggc	aaaattatca	gtgaattctc	taagtccagac	aggtgggagt	1620
ctgtatatgg	aagctgggag	tacattggat	tttgaactc	cacaaccacc	acaacagcct	1680
cctgcccgtc	atcagtcgat	cacgctttcc	aatctgcatt	tgtctctttc	ttctttgtta	1740
gcaaacaatg	cagttacgaa	tcctcctacc	aatcctccag	cgcaagattc	tcattcctgca	1800
gtcattggta	gcacaactgc	tggttctggt	acaattagtg	ggcctatctt	ttttgaggat	1860
ttggatgata	cagcttatga	taggtatgat	tggctaggtt	ctaatacaaaa	aatcgatgtc	1920
ctgaaattac	agttagggac	tcagccccc	gctaattgcc	catcagattt	gactctaggg	1980
aatgagatgc	ctaagtatgg	ctatcaagga	agctggaagc	ttgcgtggga	tcctaataca	2040
gcaaataatg	gtcctttatac	tctgaaagct	acatgacta	aaactgggta	taatcctggg	2100
cctgagcgag	tagcttcttt	ggttccaaat	agttttatgg	gatccatttt	agatatacga	2160
tctgcgcatt	cagcaattca	agcaagtgtg	gatgggcgct	cttattgtcg	aggattatgg	2220
gtttctggag	tttcgaattt	cttctatcat	gaccgcgatg	ctttagggtc	gggatatcgg	2280
tatattagtg	ggggttatte	cttaggagca	aactcctact	ttggatcatc	gatgtttggt	2340
ctagcattta	ctgaagtatt	tggtagatct	aaagattatg	tagtgtgtcg	ttccaatcat	2400
catgcttgca	taggatccgt	ttatctatct	accaaacagg	ctttatgtgg	atcttatgtg	2460
tttgagatg	gtcttattcg	tgctagctac	gggtttggga	atcagcatat	gaaaacctca	2520
tatacatttg	cagaggagag	cgatgtttgt	tgggataata	actgtctggt	tggagagatt	2580
ggagtgggat	taccgattgt	gattactcca	tctaagctct	atttgaatga	gttgcgtcct	2640
ttcgtgcaag	ctgagttttc	ttatgccgat	catgaatctt	ttacagagga	aggcgatcaa	2700
gctcgggcat	tcaggagtgg	acatctcatg	aatctatcag	ttcctgttgg	agtaaaaattt	2760
gatcgatggt	ctagtagaca	ccctaataaa	tatagcttta	tgggggctta	tatctgtgat	2820
gcttatcgca	ccatctctgg	gactcagaca	acactcctat	cccatcaaga	gacatggaca	2880
acagatgcct	ttcattttggc	aagacatgga	gtcatagtta	gaggggtctat	gtatgcttct	2940
ctaacaagca	atatagaagt	atatggccat	ggaagatatg	agtatcgaga	tacttctcga	3000
ggttatgggt	tgagtgcagg	aagtaaagtc	cggttctaaa	aatattgggt	agatagttaa	3060
gtgttagcga	tgccctttttc	tttgagatct	acatcatttt	gttttttagc	ttgtttgtgt	3120
tcctattcgt	atggattcgc	gagctctcct	caagtgttaa	cacctaatgt	aaccactcct	3180
tttaaggggg	acgatgttta	cttgaatgga	gactgcgctt	ttgtcaatgt	ctatgcaggg	3240
gcagagaacg	gctcaattat	ctcagctaata	ggcgacaatt	taacgattac	cggacaaaac	3300
catacattat	cattttacaca	ttctcaaggg	ccagttcttc	aaaattagcc	ttca	3354

<210> 24
 <211> 3324
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 24

atgcaaacgt	ctttccataa	gttcttttctt	tcaatgattc	tagcttattc	ttgctgctct	60
ttaagtggg	gggggtatgc	agcagaaatc	atgattcctc	aaggaattta	cgatggggag	120
acgttaactg	tatcatttcc	ctatactgtt	ataggagatc	cgagtgggac	tactgttttt	180
tctgcaggag	agttaacgtt	aaaaaatctt	gacaattcta	ttgcagcttt	gcctttaagt	240
tgttttggga	acttattagg	gagttttact	gttttaggga	gaggacactc	gttgactttc	300
gagaacatac	ggacttctac	aaatggagct	gcactaagtg	acagcgctaa	tagcgggtta	360
tttactattg	agggttttaa	agaattatct	ttttccaatt	gcaactcatt	acttgccgta	420
ctgcctgctg	caacgactaa	taatggtagc	cagactccga	cgacaacatc	tacaccgtct	480
aatgggtacta	tttattctaa	aacagatctt	ttgttactca	ataatgagaa	gttctcattc	540
tatagtaatt	tagtctctgg	agatggggga	actatagatg	ctaagagctt	aacggttcaa	600
ggaattagca	agctttgtgt	cttccaagaa	aatactgctc	aagctgatgg	gggagcttgt	660
caagtagtca	ccagtttctc	tgctatggct	aacgaggctc	ctattgcctt	tatagcgaat	720
gttgccaggag	taagaggggg	agggattgct	gctgttcagg	atgggcagca	gggagtgtca	780
tcactactct	caacagaaga	tccagtagta	agtttttcca	gaaatactgc	ggtagagtgt	840
gatgggaacg	tagcccaggt	aggaggaggg	atttactcct	acgggaacgt	tgctttcctg	900
aataatggaa	aaacctgtgt	tctcaacaat	gttgcttctc	ctgtttacat	tgctgctgag	960
caaccaacaa	atggacaggc	ttctaatacg	agtgataatt	acggagatgg	aggagctatc	1020
ttctgtaaga	atggtgcgca	agcagcagga	tccaataact	ctggatcagt	ttcctttgat	1080
ggagagggag	tagtttttct	tagtagcaat	gtagtctctg	ggaaaggggg	agctattttat	1140
gccccaaaagc	tctcggttgc	taactgtggc	ctgttacaat	tcttagggaa	tatcgctaat	1200
gatggtggag	cgattttatt	aggagaatct	ggagagctca	gtttatctgc	tgattatgga	1260
gatattattt	tcgatgggaa	tcttaaaaga	acagccaaag	agaatgctgc	cgatgttaat	1320
ggcgtaactg	tgctctcaca	agccatttct	atgggatcgg	gagggaaaaa	aacgcacatta	1380
agagctaaag	cagggcatca	gatttctctt	aatgatccca	tcgagatggc	aaacggaaat	1440
aaccagccag	cgcagtcttc	cgaacctcta	aaaattaacg	atggtgaagg	atacacaggg	1500
gatattgttt	ttgctaattg	aaacagtact	ttgtaccaaa	atgttacgat	agagcaagga	1560
aggattgttc	ttcgtgaaaa	ggcaaaatta	tcagtgaatt	ctctaagtca	gacaggtggg	1620
agtctgtata	tggaagctgg	gagtacattg	gattttgtaa	ctccacaacc	accacaacag	1680
cctcctgccg	ctaatacagt	gatacagctt	tccaatctgc	atttgtctct	ttcttctttg	1740
ttagcaaaaca	atgcagttac	gaatcctcct	accaatcctc	cagcgcaaga	ttctcatcct	1800
gcagtcattg	gtagcacaac	tgctggctct	gtcacaatta	gtgggccttt	cttttttgag	1860
gatttggaat	atacagctta	tgataggtat	gattggctag	gttctaatac	aaaaatcgat	1920
gtcctgaaat	tacagttagg	gactcagccc	tcagctaatt	ccccatcaga	tttgactcta	1980
gggaatgaga	tgccctaagta	tggtatcaaa	ggaagctgga	agcttgctgt	ggatcctaata	2040
acagcaaata	atggctctta	tactctgaaa	gctacatgga	ctaaaactgg	gtataatcct	2100
gggcctgagc	gagtagcttc	tttggttcca	aatagtttat	ggggatccat	tttagatata	2160
cgatctgcgc	attcagcaat	tcaagcaagt	gtggatgggc	gctcttattg	tcgaggatta	2220
tgggtttctg	gagtttcgaa	tttctcctat	catgaccgcg	atgctttagg	tcagggatata	2280
cggtatatta	gtgggggtta	ttccttagga	gcaaaactcct	actttggatc	atcgatgttt	2340
ggtctagcat	ttaccgaagt	atttggtaga	tctaaagatt	atgtagtgtg	tcgttccaat	2400
catcatgctt	gcataggatc	cgtttatcta	tctaccaaac	aagctttatg	tggtatcctat	2460
ttgttcggag	atgcgtttat	ccgtgctagc	tacgggtttg	ggaaccagca	tatgaaaacc	2520
tcatacacat	ttgcagagga	gagcgatgtt	cgttgggata	ataactgtct	ggttgagagag	2580
attggagtgg	gattaccgat	tggtgactact	ccatctaagc	tctatttgaa	tgagttgcgt	2640
cctttcgtgc	aagctgagtt	ttcttatgcc	gatcatgaat	cttttacaga	ggaaggcgat	2700
caagctcggg	cattcaggag	tggtcatctc	atgaatctat	cagttcctgt	tgtagtaaaa	2760
tttgatcgat	gttctagtac	acaccctaata	aaatatagct	ttatgggggc	ttatatctgt	2820
gatgcttatc	gcaccatctc	tgggactcag	acaacactcc	tatcccatca	agagacatgg	2880
acaacagatg	ccttttcattt	ggcaagacat	ggagtcatag	ttagaggggc	tatgtatgct	2940
tctctaacaa	gcaatataga	agtatatggc	catgggaagt	atgagtatcg	agatacttct	3000
cgaggttatg	gtttgagctgc	aggaagtata	tccgggttct	aaaaatattg	gttagatagt	3060
taagtgtttg	cgatgccttg	ttctttgaga	tctacatcat	tttggttttt	agcttggttg	3120
tgttcctatt	cgtatggatt	cgcgagctct	cctcaagtgt	taacaccta	tgtaaccact	3180
ccttttaagg	gggacgatgt	ttacttgaat	ggagactgcg	ctttagtcaa	tgtctatgca	3240
ggggcagaga	acggctcaat	tatctcagct	aatggcgaca	atttaacgat	taccggacaa	3300
aaccatgcat	tatcattttac	agat				3324

<210> 25

<211> 65

<212> PRT
<213> Chlamydia sp.

<400> 25
Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
1 5 10 15
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu
20 25 30
Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly
35 40 45
His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala
50 55 60

Leu

65

<210> 26
<211> 24
<212> PRT
<213> Chlamydia sp.

<400> 26
Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser
1 5 10 15
Ser Leu Leu Ala Asn Asn Ala Val
20

<210> 27
<211> 8
<212> PRT
<213> Chlamydia sp.

<400> 27
Gly Tyr Thr Gly Asp Ile Val Phe
1 5

<210> 28
<211> 7
<212> PRT
<213> Chlamydia sp.

<400> 28
Tyr Gly Asp Ile Ile Phe Asp
1 5

<210> 29
<211> 63
<212> PRT
<213> Chlamydia sp.

<400> 29
Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu
1 5 10 15
Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly
20 25 30
Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn
35 40 45
Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly
50 55 60

<210> 30
<211> 22
<212> PRT
<213> Chlamydia sp.

<400> 30
Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys
1 5 10 15

Ile Asn Asp Gly Glu Gly
20

<210> 31
<211> 14
<212> PRT
<213> Chlamydia sp.

<400> 31
Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu
1 5 10
<210> 32
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 32
Lys Leu Ser Val Asn Ser Leu Ser Gln Thr
1 5 10
<210> 33
<211> 45
<212> PRT
<213> Chlamydia sp.

<400> 33
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu
35 40 45
<210> 34
<211> 64
<212> PRT
<213> Chlamydia sp.

<400> 34
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys
35 40 45
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro
50 55 60
<210> 35
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 35
Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
1 5 10
<210> 36
<211> 458
<212> PRT
<213> Chlamydia sp.

<400> 36
Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu
1 5 10 15
Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly
20 25 30

Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile
 20 25 30
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 35 40 45
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp
 50 55 60
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 85 90 95
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 100 105 110
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu
 115 120 125
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 130 135 140
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 145 150 155 160
 Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly
 165 170 175
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 180 185 190
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 195 200 205
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn
 210 215 220
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 225 230 235 240
 Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg
 245 250 255
 Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 260 265 270
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly
 275 280 285
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 290 295 300
 Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 305 310 315 320
 Ser Arg Val Arg Phe
 325

<210> 38
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 38
 000

3

<210> 39
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 39
 000

<210> 40
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 40
 000
 <210> 41
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 41
 000
 <210> 42
 <211> 6
 <212> PRT
 <213> Chlamydia sp.

<400> 42
 Glu Ile Met Val Pro Gln
 1 5
 <210> 43
 <211> 984
 <212> PRT
 <213> Chlamydia sp.

<400> 43
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
 1 5 10 15
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300

Asn	Tyr	Gly	Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala
305					310					315					320
Gly	Ser	Asn	Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val
				325					330					335	
Phe	Phe	Ser	Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala
				340				345					350		
Lys	Lys	Leu	Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn
		355					360					365			
Ile	Ala	Asn	Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu
	370					375					380				
Ser	Leu	Ser	Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys
385					390					395					400
Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser
				405					410					415	
Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg
			420					425					430		
Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala
		435					440					445			
Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu	Leu	Lys	Ile	Asn
	450					455					460				
Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Ser	Ser
465					470					475					480
Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg
				485				490						495	
Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser
			500					505					510		
Leu	Tyr	Met	Glu	Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val	Thr	Pro	Gln	Pro
		515					520					525			
Pro	Gln	Gln	Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu
	530					535					540				
His	Leu	Ser	Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro
545					550					555					560
Pro	Thr	Asn	Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser
				565					570					575	
Thr	Thr	Ala	Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp
			580					585					590		
Leu	Asp	Asp	Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln
		595					600					605			
Lys	Ile	Asn	Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys	Pro	Pro	Ala	Asn
	610					615					620				
Ala	Pro	Ser	Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr
625					630					635					640
Gln	Gly	Ser	Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly
				645					650					655	
Pro	Tyr	Thr	Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly
			660					665					670		
Pro	Glu	Arg	Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile
		675					680					685			
Leu	Asp	Ile	Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly
	690					695					700				
Arg	Ser	Tyr	Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe
705					710					715					720
Tyr	His	Asp	Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly
				725					730					735	
Gly	Tyr	Ser	Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly
			740					745					750		
Leu	Ala	Phe	Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys
		755					760					765			
Arg	Ser	Asn	His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Gln
	770					775					780				
Gln	Ala	Leu	Cys	Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala
785					790					795					800

Ser	Tyr	Gly	Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala
				805					810					815	
Glu	Glu	Ser	Asp	Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Ala	Gly	Glu	Ile
			820					825					830		
Gly	Ala	Gly	Leu	Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn
		835					840					845			
Glu	Leu	Arg	Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His	Glu
	850					855					860				
Ser	Phe	Thr	Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Lys	Ser	Gly	His
865					870					875					880
Leu	Leu	Asn	Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys	Ser
			885						890					895	
Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met	Ala	Ala	Tyr	Ile	Cys	Asp
			900					905					910		
Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr	Thr	Leu	Leu	Ser	His	Gln
		915					920					925			
Glu	Thr	Trp	Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val	Val
	930					935					940				
Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val	Tyr
945					950					955					960
Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala	Ser	Arg	Gly	Tyr	Gly	Leu
			965						970					975	
Ser	Ala	Gly	Ser	Arg	Val	Arg	Phe								
			980												